

SEQUENCE LISTING

<110> MARKAU, URSULA

EBENBICHLER, CHRISTINE

ACHHAMMER, GUNTAR

ANKENBAUER, WALTRAUD

<120> MODIFIED DNA-POLYMERASE FROM CARBOXYDOTHENUS HYDROGENOFORMANS AND ITS USE FOR COUPLED REVERSE TRANSCRIPTION AND POLYMERASE CHAIN REACTION

<130> 1803-332-999

<150> 09/204,208

<151> 1998-12-01

<150> EP 97121151.1

<151> 1997-12-02

<160> 12

<170> PatentIn version 3.0

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<223> Description of artificial sequence: amplification primer

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 tta gct aca atc ctg cgg gaa ata ccg tta gaa atc tcc ctg gaa gat 96
 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
 20 25 30
 tta aaa gtt aaa gaa cct aat tat gaa gaa gtt gct aaa tta ttt ctt 144
 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu

35	40	45	
cac ctt gag ttt aaa agc ttt tta aaa gaa ata gaa cca aaa ata aag His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys 50 55 60			192
aaa gaa tac cag gaa ggt aaa gat ttg gtg caa gtt gaa act gta gaa Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu 65 70 75 80			240
acg gaa gga cag att gca gta gtt ttt agt gat gga ttt tat gtt gat Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp 85 90 95			288
gac ggg gaa aaa aca aag ttt tac tct tta gac cgg ctg aat gaa ata Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile 100 105 110			336
gag gaa ata ttt agg aat aaa aaa att att acc gac gat gcc aaa gga Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly 115 120 125			384
att tat cat gtc tgt tta gaa aaa ggt ctg act ttt ccc gaa gtt tgt Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys 130 135 140			432
ttt gat gcg cgg att gca gct tat gtt tta aac ccg gcc gac caa aat Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn 145 150 155 160			480
ccc ggc ctc aag ggg ctt tat cta aag tat gac tta ccg gtg tat gaa Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu 165 170 175			528
gat gta tct tta aac att aga ggg ttg ttt tat tta aaa aaa gaa atg Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met 180 185 190			576
atg aga aaa atc ttt gag cag gag caa gaa agg tta ttt tat gaa ata Met Arg Lys Ile Phe Glu Gln Glu Gln Glu Arg Leu Phe Tyr Glu Ile 195 200 205			624
gaa ctt cct tta act cca gtt ctt gct caa atg gag cat acc ggc att Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile 210 215 220			672
cag gtt gac cgg gaa gct tta aaa gag atg tcg tta gag ctg gga gag Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu 225 230 235 240			720
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ctt ggg ctg ccg gta att aaa aag acc aaa acg ggc tac tct acc gat Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp 275 280 285			864
gcg gag gtt ttg gaa gag ctc ttg cct ttc cac gaa att atc ggc aaa Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys 290 295 300			912

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 Ile Leu Asn Tyr Arg Gln Leu Met Lys Leu Lys Ser Thr Tyr Thr Asp
 305 310 315 320

ggc tta atg cct tta ata aat gag cgt acc ggt aaa ctt cac act act 1008
 Gly Leu Met Pro Leu Ile Asn Glu Arg Thr Gly Lys Leu His Thr Thr
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ttt aac cag acc ggt act tta acc gga cgc ctg gcg tct tcg gag ccc 1056
 Phe Asn Gln Thr Gly Thr Leu Thr Gly Arg Leu Ala Ser Ser Glu Pro
 340 345 350

aat ctc caa aat att ccc atc cgg ttg gaa ctc ggt cgg aaa tta cgc 1104
 Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Leu Gly Arg Lys Leu Arg
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aag atg ttt ata cct tca ccg ggg tat gat tat att gtt tcg gcg gat 1152
 Lys Met Phe Ile Pro Ser Pro Gly Tyr Asp Tyr Ile Val Ser Ala Asp
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tat tcc cag att gaa tta agg ctt ctt gcc cat ttt tcc gaa gag ccc 1200
 Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His Phe Ser Glu Glu Pro
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aag ctt att gaa gct tac caa aaa ggg gag gat att cac cgg aaa acg 1248
 Lys Leu Ile Glu Ala Tyr Gln Lys Gly Glu Asp Ile His Arg Lys Thr
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gcc tcc gag gtg ttc ggt gta tct ttg gaa gaa gtt act ccc gag atg 1296
 Ala Ser Glu Val Phe Gly Val Ser Leu Glu Glu Val Thr Pro Glu Met
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 Arg Ala His Ala Lys Ser Val Asn Phe Gly Ile Val Tyr Gly Ile Ser
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gat ttt ggt tta ggc aga gac tta aag att ccc cgg gag gtt gcc ggt 1392
 Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
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aag tac att aaa aat tat ttt gcc aac tat ccc aaa gtg cgg gag tat 1440
 Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
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ctc gat gaa ctt gtc cgt acg gca aga gaa aag gga tat gtg acc act 1488
 Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
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tta ttt ggg cga aga cgc tat att cct gag cta tct tca aaa aac cgc 1536
 Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
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acg gtt cag ggt ttt ggc gaa agg acg gcc atg aat act ccc ctt cag 1584
 Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
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ggc tcg gct gcc gat att att aag ctt gca atg att aat gta gaa aaa 1632
 Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
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gaa ctt aaa gcc cgt aag ctt aag tcc cgg ctc ctt ctt tcg gtg cac 1680
 Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His

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545	550	555	560	
gat gag tta gtt tta gaa gtg ccg gcg gaa gag ctg gaa gag gta aaa				1728
Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys	565	570	575	
gcg ctg gta aaa ggg gtt atg gag tcg gtg gtt gaa ctg aaa gtg cct				1776
Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro	580	585	590	
tta atc gct gaa gtt ggt gca ggc aaa aac tgg tat gaa gcg aag taa				1824
Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys	595	600	605	

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<213> Carboxydotherrnus hydrogenoformans

<400> 11

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Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
20 25 30

Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
35 40 45

His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
50 55 60

Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
65 70 75 80

Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
85 90 95

Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile
100 105 110

Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly
115 120 125

Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys
130 135 140

Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn

145		150		155		160
Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu						
		165		170		175
Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met						
		180		185		190
Met Arg Lys Ile Phe Glu Gln Glu Gln Glu Arg Leu Phe Tyr Glu Ile						
		195		200		205
Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile						
		210		215		220
Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu						
		225		230		235
Gln Ile Glu Glu Leu Ile Arg Glu Ile Tyr Val Leu Ala Gly Glu Glu						
		245		250		255
Phe Asn Leu Asn Ser Pro Arg Gln Leu Gly Val Ile Leu Phe Glu Lys						
		260		265		270
Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp						
		275		280		285
Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys						
		290		295		300
Ile Leu Asn Tyr Arg Gln Leu Met Lys Leu Lys Ser Thr Tyr Thr Asp						
		305		310		315
Gly Leu Met Pro Leu Ile Asn Glu Arg Thr Gly Lys Leu His Thr Thr						
		325		330		335
Phe Asn Gln Thr Gly Thr Leu Thr Gly Arg Leu Ala Ser Ser Glu Pro						
		340		345		350
Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Leu Gly Arg Lys Leu Arg						
		355		360		365
Lys Met Phe Ile Pro Ser Pro Gly Tyr Asp Tyr Ile Val Ser Ala Asp						
		370		375		380
Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His Phe Ser Glu Glu Pro						
		385		390		395
Lys Leu Ile Glu Ala Tyr Gln Lys Gly Glu Asp Ile His Arg Lys Thr						

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Ala Ser Glu Val Phe Gly Val Ser Leu Glu Glu Val Thr Pro Glu Met
420 425 430

Arg Ala His Ala Lys Ser Val Asn Phe Gly Ile Val Tyr Gly Ile Ser
435 440 445

Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
450 455 460

Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
465 470 475 480

Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
485 490 495

Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
500 505 510

Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
515 520 525

Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
530 535 540

Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His
545 550 555 560

Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys
565 570 575

Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro
580 585 590

Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys
595 600 605

<210> 12

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: amplification primer

[illegible]